ABSTRACT

[130]   There is a pressing need for computer-implemented tools that can summarize and present the enormous amounts of public literature to facilitate analysis of gene expression data. The present invention provides techniques and systems for efficiently integrating public literature regarding gene function with data from gene expression profiling experiments. Information from literature databases relating to a particular set of DNA sequences of known expression pattern is retrieved, processed, cross-referenced and viewed to provide further information about a particular DNA sequence to facilitate its identification as a candidate gene.